

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/532,683
Source: 1Fwp
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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/532,683

DATE: 08/02/2006

TIME: 08:46:46

Input Set : A:\2005_0716A Sequence.txt
 Output Set: N:\CRF4\08022006\J532683.raw

3 <110> APPLICANT: Ishihara Sangyo Kaisha, Ltd.
 5 <120> TITLE OF INVENTION: Regulation of RAPL-Rap1 Interaction
 7 <130> FILE REFERENCE: IS-08PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/532,683
 C--> 9 <141> CURRENT FILING DATE: 2005-04-26
 9 <150> PRIOR APPLICATION NUMBER: JP 2002-316892
 10 <151> PRIOR FILING DATE: 2002-10-30
 12 <160> NUMBER OF SEQ ID NOS: 14
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 555
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (1)..(555)
 24 <223> OTHER INFORMATION: Human Rap1
 27 <400> SEQUENCE: 1

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32 tct gct ctg aca gtt cag ttt gtt cag gga att ttt gtt gaa aaa tat	96
33 Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr	
34 20 25 30	
36 gac cca acg ata gaa gat tcc tac aga aag caa gtt gaa gtc gat tgc	144
37 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys	
38 35 40 45	
40 caa cag tgt atg ctc gaa atc ctg gat act gca ggg aca gag caa ttt	192
41 Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe	
42 50 55 60	
44 aca gca atg agg gat ttg tat atg aag aac ggc caa ggt ttt gca cta	240
45 Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu	
46 65 70 75 80	
48 gta tat tct att aca gct cag tcc acg ttt aac gac tta cag gac ctg	288
49 Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu	
50 85 90 95	
52 agg gaa cag att tta cgg gtt aag gac acg gaa gat gtt cca atg att	336
53 Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile	
54 100 105 110	
56 ttg gtt ggc aat aaa tgt gac ctg gaa gat gag cga gta gtt ggc aaa	384
57 Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys	
58 115 120 125	
60 gag cag ggc cag aat tta gca aga cag tgg tgt aac tgt gcc ttt tta	432

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62	130					135						140					
64	gaa	tct	tct	gca	aag	tca	aag	atc	aat	gtt	aat	gag	ata	ttt	tat	gac	480
65	Glu	Ser	Ser	Ala	Lys	Ser	Lys	Ile	Asn	Val	Asn	Glu	Ile	Phe	Tyr	Asp	
66	145					150					155					160	
68	ctg	gtc	aga	cag	ata	aat	agg	aaa	aca	cca	gtg	gaa	aag	aag	aag	cct	528
69	Leu	Val	Arg	Gln	Ile	Asn	Arg	Lys	Thr	Pro	Val	Glu	Lys	Lys	Pro		
70						165				170					175		
72	aaa	aag	aaa	tca	tgt	ctg	ctg	ctc	tag								555
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88	Ser	Ala	Leu	Thr	Val	Gln	Phe	Val	Gln	Gly	Ile	Phe	Val	Glu	Lys	Tyr	
89						20				25						30	
92	Asp	Pro	Thr	Ile	Glu	Asp	Ser	Tyr	Arg	Lys	Gln	Val	Glu	Val	Asp	Cys	
93						35				40						45	
96	Gln	Gln	Cys	Met	Leu	Glu	Ile	Leu	Asp	Thr	Ala	Gly	Thr	Glu	Gln	Phe	
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101	65					70				75						80	
104	Val	Tyr	Ser	Ile	Thr	Ala	Gln	Ser	Thr	Phe	Asn	Asp	Leu	Gln	Asp	Leu	
105						85				90						95	
108	Arg	Glu	Gln	Ile	Leu	Arg	Val	Lys	Asp	Thr	Glu	Asp	Val	Pro	Met	Ile	
109						100				105						110	
112	Leu	Val	Gly	Asn	Lys	Cys	Asp	Leu	Glu	Asp	Glu	Arg	Val	Val	Gly	Lys	
113						115				120						125	
116	Glu	Gln	Gly	Gln	Asn	Leu	Ala	Arg	Gln	Trp	Cys	Asn	Cys	Ala	Phe	Leu	
117						130				135						140	
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121	145					150				155						160	
124	Leu	Val	Arg	Gln	Ile	Asn	Arg	Lys	Thr	Pro	Val	Glu	Lys	Lys	Pro		
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140	<223>	OTHER INFORMATION:	Human RAPL (or Human p30)														
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Input Set : A:\2005_0716A_Sequence.txt
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149 Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn	
150 20 25 30	
152 gcg cag agc aaa cat ctt tca aag aat gtc tgt aaa cct gtc gag gaa	144
153 Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu	
154 35 40 45	
156 aca cag cgc ccg ccc aca ctg cag gag atc aag cag aag atc gac agc	192
157 Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser	
158 50 55 60	
160 tac aac acg cga gag aag aac tgc ctg ggc atg aaa ctg agt gaa gac	240
161 Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp	
162 65 70 75 80	
164 ggc acc tac acg ggt ttc atc aaa gtc cat ctg aaa ctc cgg cgg cct	288
165 Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro	
166 85 90 95	
168 gtg acg gtg cct gct ggg atc cgg ccc cag tcc atc tat gat gcc atc	336
169 Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile	
170 100 105 110	
172 aag gag gtg aac ctg gcg gct acc acg gac aag cgg aca tcc ttc tac	384
173 Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr	
174 115 120 125	
176 ctg ccc cta gat gcc atc aag cag ctg cac atc agc agc acc acc acc	432
177 Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr	
178 130 135 140	
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181 Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp	
182 145 150 155 160	
184 aat ccc cag aag ttt gca ctt ttt aag cgg ata cac aag gac gga caa	528
185 Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln	
186 165 170 175	
188 gtg ctc ttc cag aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc	576
189 Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg	
190 180 185 190	
192 ctg ctt gct ggg cct gac acg gag gtc ctc agc ttt gtc cta aag gag	624
193 Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu	
194 195 200 205	
196 aat gaa act gga gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt	672
197 Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu	
198 210 215 220	
200 cag aac ttc cta aca atc ctg gaa aaa gag gag cag gac aaa atc caa	720
201 Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln	
202 225 230 235 240	
204 caa gtg caa aag aag tat gac aag ttt agg cag aaa ctg gag gag gcc	768
205 Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala	
206 245 250 255	
208 tta aga gaa tcc cag ggc aaa cct ggg taa	798

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Input Set : A:\2005_0716A_Sequence.txt
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214 <211> LENGTH: 265
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
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221 1          5          10          15
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228 Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu
229          35          40          45
232 Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser
233          50          55          60
236 Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp
237 65          70          75          80
240 Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro
241          85          90          95
244 Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile
245          100         105         110
248 Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr
249          115         120         125
252 Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr
253          130         135         140
256 Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp
257 145         150         155         160
260 Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln
261          165         170         175
264 Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg
265          180         185         190
268 Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu
269          195         200         205
272 Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu
273          210         215         220
276 Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln
277 225         230         235         240
280 Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala
281          245         250         255
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285          260         265
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289 <211> LENGTH: 498
290 <212> TYPE: DNA
291 <213> ORGANISM: Homo sapiens
293 <220> FEATURE:
294 <221> NAME/KEY: CDS
295 <222> LOCATION: (1)..(498)
296 <223> OTHER INFORMATION: Dominant-Negative Human RAPL

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RAW SEQUENCE LISTING

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Input Set : A:\2005_0716A_Sequence.txt
 Output Set: N:\CRF4\08022006\J532683.raw

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 302 1 5 10 15
 304 ctg gcg gct acc acg gac aag cgg aca tcc ttc tac ctg ccc cta gat 96
 305 Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
 306 20 25 30
 308 gcc atc aag cag ctg cac atc agc acc acc acc gtc agt gag gtc 144
 309 Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Val Ser Glu Val
 310 35 40 45
 312 atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac aat ccc cag aag 192
 313 Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
 314 50 55 60
 316 ttt gca ctt ttt aag cgg ata cac aag gac gga caa gtg ctc ttc cag 240
 317 Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
 318 65 70 75 80
 320 aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc ctg ctt gct ggg 288
 321 Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg Leu Leu Ala Gly
 322 85 90 95
 324 cct gac acg gag gtc ctc agc ttt gtg cta aag gag aat gaa act gga 336
 325 Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu Asn Glu Thr Gly
 326 100 105 110
 328 gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt cag aac ttc cta 384
 329 Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu Gln Asn Phe Leu
 330 115 120 125
 332 aca atc ctg gaa aaa gag gag cag gac aaa atc caa caa gtg caa aag 432
 333 Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln Gln Val Gln Lys
 334 130 135 140
 336 aag tat gac aag ttt agg cag aaa ctg gag gag gcc tta aga gaa tcc 480
 337 Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala Leu Arg Glu Ser
 338 145 150 155 160
 340 cag ggc aaa cct ggg taa 498
 341 Gln Gly Lys Pro Gly
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 346 <211> LENGTH: 165
 347 <212> TYPE: PRT
 348 <213> ORGANISM: Homo sapiens
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 356 Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
 357 20 25 30
 360 Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Val Ser Glu Val
 361 35 40 45
 364 Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
 365 50 55 60
 368 Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
 369 65 70 75 80

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/532,683

DATE: 08/02/2006

TIME: 08:46:47

Input Set : A:\2005_0716A_Sequence.txt

Output Set: N:\CRF4\08022006\J532683.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date